

Appendix III

Alignment of SEQ ID NO: 1479 of Tang et al with the sequence of GenBank Accession No. BAA23691.2

>gb|BAA23691.2| KIAA0395 [Homo sapiens]
Length=879

Score = 1827 bits (4732), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 877/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%)

Query	78	SCKYCDPRSHDMTOFVGHMNSHHTDFNKDPTFVCSGCSFLAKTEPEGLSLHMATCHSGEAS	137
Sbjct	1	SCKYCDPRSHDMTOFVGHMNSHHTDFNKDPTFVCSGCSFLAKTEPEGLSLHMATCHSGEAS	60
Query	138	FVMNVAKPDNHVVVEQSIPBSTSTPDLAGEPSAEGADGOAEIIITKTPIMKIMKGKAEAK	197
Sbjct	61	FVMNVAKPDNHVVVEQSIPBSTSTPDLAGEPSAEGADGOAEIIITKTPIMKIMKGKAEAK	120
Query	198	KIHTLKENVPSQPVGAEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGPL	257
Sbjct	121	KIHTLKENVPSQPVGAEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGPL	180
Query	258	IGTVFLPAGIAQFLSLQQQPFVHAQHVVHQELPTAKALPKVMIPLSSIPTTSAAMDNS	317
Sbjct	181	IGTVFLPAGIAQFLSLQQQPFVHAQHVVHQELPTAKALPKVMIPLSSIPTTSAAMDNS	240
Query	318	FLKNSFHKKFPYPTKAECLYLTVVTKYPEEQLKIWPTAQLKQGISMSPEIEHAPKMFN	377
Sbjct	241	FLKNSFHKKFPYPTKAECLYLTVVTKYPEEQLKIWPTAQLKQGISMSPEIEHAPKMFN	300
Query	378	TVIQSVPOPTITVLNTPILVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTPQLMANGQL	437
Sbjct	301	TVIQSVPOPTITVLNTPILVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTPQLMANGQL	360
Query	438	ATSSLEPLIVTSVFKQPGVAPINTVCSNTTSAVKVYVNAQOSLLTACPSITSOAFLDASII	497
Sbjct	361	ATSSLEPLIVTSVFKQPGVAPINTVCSNTTSAVKVYVNAQOSLLTACPSITSOAFLDASII	420
Query	498	KKKSHQQLSALKGSPCRNQFFGQSEVEHLTKVTGLSTREVRKMPSDRRYHCRNLKGSRA	557
Sbjct	421	KKKSHQQLSALKGSPCRNQFFGQSEVEHLTKVTGLSTREVRKMPSDRRYHCRNLKGSRA	480
Query	558	MIPGDHSSIIDSVPVPSFSPSSKVPVETCIPPTATLATHPSAKRQSMHQTPDPTTKYK	617
Sbjct	481	MIPGDHSSIIDSVPVPSFSPSSKVPVETCIPPTATLATHPSAKRQSMHQTPDPTTKYK	540
Query	618	ERAPQLRALSSSTAQNPLPLDERLDPLRSETKMTREIDSWFSERRKKVNAEETTKAEZ	677
Sbjct	541	ERAPQLRALSSSTAQNPLPLDERLDPLRSETKMTREIDSWFSERRKKVNAEETTKAEZ	600
Query	678	NASQEEEEAADEGGEDLASLRLVSGENGSLMPSSHILAEKRVSPKIKILNKLRLVTEA	737
Sbjct	601	NASQEEEEAADEGGEDLASLRLVSGENGSLMPSSHILAEKRVSPKIKILNKLRLVTEA	660
Query	738	NGRNEIPGLGACDPEDDESNIARQLPGKVSCKKTAQQRHLLRLQFLVQPMNSHQDYLSI	797
Sbjct	661	NGRNEIPGLGACDPEDDESNIARQLPGKVSCKKTAQQRHLLRLQFLVQPMNSHQDYLSI	720
Query	798	MAQTGLPRPEVVMFGDSRYALNGQLKWYEDYKGNFPGGLLVIAFGHRLQLQDYTMTH	857
Sbjct	721	MAQTGLPRPEVVMFGDSRYALNGQLKWYEDYKGNFPGGLLVIAFGHRLQLQDYTMTH	780
Query	858	KMLYEEDLQMLCDKTQSSQGVKQWFAEKMGHEETRAVADTGSFQGGTGLDVAHKGMS	917
Sbjct	781	KMLYEEDLQMLCDKTQSSQGVKQWFAEKMGHEETRAVADTGSFQGGTGLDVAHKGMS	840
Query	918	DTYSEVSENSSESWEPVPEASSEFPDTSSPQAGRQLETD	956
Sbjct	841	DTYSEVSENSSESWEPVPEASSEFPDTSSPQAGRQLETD	879